

10347-WO-ST25
SEQUENCE LISTING

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<120> Method of Preparing an Edible Product

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<170> PatentIn version 3.2

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 tctccagtct ctccaagtgt tgtgccctct tgtgttagcc cagc atg tcg ccc tct 116
 Met Ser Pro Ser
 1
 ttc cac tcc cta ctc gct atc gca acc ctt gca ggc tca gct gcc ctt 164
 Phe His Ser Leu Leu Ala Ile Ala Thr Leu Ala Gly Ser Ala Ala Leu
 5 10 15 20
 gca tcc ccg atc ccg gag cca gaa aca ccg cag ctt atc ccc cgg gct 212
 Ala Ser Pro Ile Pro Glu Pro Glu Thr Pro Gln Leu Ile Pro Arg Ala
 25 30 35
 gtt ggt gac ttt gag tgc ttc aac gct agt ctt ccc aac atc acc atc 260
 Val Gly Asp Phe Glu Cys Phe Asn Ala Ser Leu Pro Asn Ile Thr Ile
 40 45 50
 ttc gcg act ggt ggt acc atc gct ggt tct gct ggt tct gcc gat cag 308
 Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Gly Ser Ala Asp Gln
 55 60 65
 act acg ggt tac cag gct ggt gca ttg ggt atc caa gcg ttg atc gac 356
 Thr Thr Gly Tyr Gln Ala Gly Ala Leu Gly Ile Gln Ala Leu Ile Asp
 70 75 80
 gct gtc ccg caa ctc tgc aac gtc tcc aac gtc agg ggt gtg cag atc 404
 Ala Val Pro Gln Leu Cys Asn Val Ser Asn Val Arg Gly Val Gln Ile
 85 90 95 100
 gcc aac gtt gat agc ggc gat gta aac tct act atc ctg acc act ttg 452
 Ala Asn Val Asp Ser Gly Asp Val Asn Ser Thr Ile Leu Thr Thr Leu
 105 110 115
 gcg cat cgc atc cag act gat ctt gac aac cct cac atc caa ggt gtt 500
 Ala His Arg Ile Gln Thr Asp Leu Asp Asn Pro His Ile Gln Gly Val
 120 125 130
 gtc gtc acc cat ggc aca gac act ctc gag gag tct tca ttt ttc ctc 548
 Val Val Thr His Gly Thr Asp Thr Leu Glu Glu Ser Ser Phe Phe Leu
 135 140 145
 gat ctc act gtc caa agt gaa aag cct gtt gtt atg gtt gga tcc atg 596
 Asp Leu Thr Val Gln Ser Glu Lys Pro Val Val Met Val Gly Ser Met
 150 155 160
 cgt cct gcc act gcc atc agc gct gat ggt ccc atc aac ctc ctg tct 644
 Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Ile Asn Leu Leu Ser
 165 170 175 180
 gct gtt cga ttg gca ggt agc aag agt gcc aag ggt cgc ggt aca atg 692
 Ala Val Arg Leu Ala Gly Ser Lys Ser Ala Lys Gly Arg Gly Thr Met
 185 190 195

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att gta ctc aac gac aag atc gct tct gca cgc tac acc gtt aaa tcc	740
Ile Val Leu Asn Asp Lys Ile Ala Ser Ala Arg Tyr Thr Val Lys Ser	
	200
	205
	210
cac gcc aat gct gtc cag act ttc att gcc gaa gat caa ggt tat ctt	788
His Ala Asn Ala Val Gln Thr Phe Ile Ala Glu Asp Gln Gly Tyr Leu	
	215
	220
	225
ggt gcc ttt gaa aac att cag ccc gtc ttc tgg tac cct gct agt cga	836
Gly Ala Phe Glu Asn Ile Gln Pro Val Phe Trp Tyr Pro Ala Ser Arg	
	230
	235
	240
cca cta ggt cac cac tat ttc aac att agt gct agc tca cct aag aag	884
Pro Leu Gly His His Tyr Phe Asn Ile Ser Ala Ser Ser Pro Lys Lys	
	245
	250
	255
	260
gct ctt cct cag gtt gac gtt ttg tac ggc cac caa gaa gcg gac ccc	932
Ala Leu Pro Gln Val Asp Val Leu Tyr Gly His Gln Glu Ala Asp Pro	
	265
	270
	275
gag ctt ttc caa gct gct gtc gat agc ggc gcc cag ggc att gtt ctc	980
Glu Leu Phe Gln Ala Ala Val Asp Ser Gly Ala Gln Gly Ile Val Leu	
	280
	285
	290
gct ggt ctt ggc gct gga ggc tgg cct gac gaa gct gct gat gag atc	1028
Ala Gly Leu Gly Ala Gly Gly Trp Pro Asp Glu Ala Ala Asp Glu Ile	
	295
	300
	305
aag aag gtc ttg aac gag act aac att cct gtt gtt gtc agc cgt cgt	1076
Lys Lys Val Leu Asn Glu Thr Asn Ile Pro Val Val Val Ser Arg Arg	
	310
	315
	320
act gct tgg ggt tac gtt gga gag agg cct ttc ggt atc ggt gct ggg	1124
Thr Ala Trp Gly Tyr Val Gly Glu Arg Pro Phe Gly Ile Gly Ala Gly	
	325
	330
	335
	340
tac ttg aac cct tcc aag gcc aga atc caa ctg caa ctt gcg ctt gag	1172
Tyr Leu Asn Pro Ser Lys Ala Arg Ile Gln Leu Gln Leu Ala Leu Glu	
	345
	350
	355
aag aag ctt tct gtg gag gag atc caa gac ata ttc gag tat gtt	1217
Lys Lys Leu Ser Val Glu Glu Ile Gln Asp Ile Phe Glu Tyr Val	
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	365
	370
tgattggaag aggattttga aatgaatcaa tgatatatga tta	1260

<210> 8
 <211> 371
 <212> PRT
 <213> Fusarium graminearum

<400> 8

Met Ser Pro Ser Phe His Ser Leu Leu Ala Ile Ala Thr Leu Ala Gly
 1 5 10 15

Ser Ala Ala Leu Ala Ser Pro Ile Pro Glu Pro Glu Thr Pro Gln Leu
 20 25 30

Ile Pro Arg Ala Val Gly Asp Phe Glu Cys Phe Asn Ala Ser Leu Pro
 35 40 45

Asn Ile Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Gly
 50 55 60

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Ser Ala Asp Gln Thr Thr Gly Tyr Gln Ala Gly Ala Leu Gly Ile Gln
 65 70 75 80
 Ala Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ser Asn Val Arg
 85 90 95
 Gly Val Gln Ile Ala Asn Val Asp Ser Gly Asp Val Asn Ser Thr Ile
 100 105 110
 Leu Thr Thr Leu Ala His Arg Ile Gln Thr Asp Leu Asp Asn Pro His
 115 120 125
 Ile Gln Gly Val Val Val Thr His Gly Thr Asp Thr Leu Glu Glu Ser
 130 135 140
 Ser Phe Phe Leu Asp Leu Thr Val Gln Ser Glu Lys Pro Val Val Met
 145 150 155 160
 Val Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Ile
 165 170 175
 Asn Leu Leu Ser Ala Val Arg Leu Ala Gly Ser Lys Ser Ala Lys Gly
 180 185 190
 Arg Gly Thr Met Ile Val Leu Asn Asp Lys Ile Ala Ser Ala Arg Tyr
 195 200 205
 Thr Val Lys Ser His Ala Asn Ala Val Gln Thr Phe Ile Ala Glu Asp
 210 215 220
 Gln Gly Tyr Leu Gly Ala Phe Glu Asn Ile Gln Pro Val Phe Trp Tyr
 225 230 235 240
 Pro Ala Ser Arg Pro Leu Gly His His Tyr Phe Asn Ile Ser Ala Ser
 245 250 255
 Ser Pro Lys Lys Ala Leu Pro Gln Val Asp Val Leu Tyr Gly His Gln
 260 265 270
 Glu Ala Asp Pro Glu Leu Phe Gln Ala Ala Val Asp Ser Gly Ala Gln
 275 280 285
 Gly Ile Val Leu Ala Gly Leu Gly Ala Gly Gly Trp Pro Asp Glu Ala
 290 295 300
 Ala Asp Glu Ile Lys Lys Val Leu Asn Glu Thr Asn Ile Pro Val Val
 305 310 315 320
 Val Ser Arg Arg Thr Ala Trp Gly Tyr Val Gly Glu Arg Pro Phe Gly
 325 330 335

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Ile Gly Ala Gly Tyr Leu Asn Pro Ser Lys Ala Arg Ile Gln Leu Gln
 340 345 350

Leu Ala Leu Glu Lys Lys Leu Ser Val Glu Glu Ile Gln Asp Ile Phe
 355 360 365

Glu Tyr Val
 370

<210> 9
 <211> 1470
 <212> DNA
 <213> *Fusarium graminearum*

<220>
 <221> CDS
 <222> (77)..(1429)

<400> 9
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 gatatcagtc tacatc atg atg ccc agc gtc aga aga ttt cac ggc cag act 112
 Met Met Pro Ser Val Arg Arg Phe His Gly Gln Thr
 1 5 10
 atg gtc gcc gcc gct cct tct att tgc tca ggg cct gca gca tcg tcc 160
 Met Val Ala Ala Ala Pro Ser Ile Cys Ser Gly Pro Ala Ala Ser Ser
 15 20 25
 acc atc aag atg gct tca tcg tca gct tcg tgg acg act tat ctg tgg 208
 Thr Ile Lys Met Ala Ser Ser Ser Ala Ser Trp Thr Thr Tyr Leu Trp
 30 35 40
 cgg ctt atc cta gct gtg ctg gct cct tca acg gcc ctg ctg cct ttt 256
 Arg Leu Ile Leu Ala Val Leu Ala Pro Ser Thr Ala Leu Leu Pro Phe
 45 50 55 60
 ggt gcg tgg gtt gtt tcg gtc tgg gga tct cct gtc ctc gac cta cac 304
 Gly Ala Trp Val Val Ser Val Trp Gly Ser Pro Val Leu Asp Leu His
 65 70 75
 gtc caa cct cac ttc tcg gtt caa caa aaa gcg cca ata cag acg ggc 352
 Val Gln Pro His Phe Ser Val Gln Gln Lys Ala Pro Ile Gln Thr Gly
 80 85 90
 atc cct ttc gaa att tcg acc acc tca gga ttc aac tgc ttc aat ccc 400
 Ile Pro Phe Glu Ile Ser Thr Thr Ser Gly Phe Asn Cys Phe Asn Pro
 95 100 105
 aat ctt ccc aac gtc act att tat gcc acc gga ggt act att gct ggc 448
 Asn Leu Pro Asn Val Thr Ile Tyr Ala Thr Gly Gly Thr Ile Ala Gly
 110 115 120
 tcc gca agc tcg gct gat cag acc acg gga tac cgg tca gct gcg tta 496
 Ser Ala Ser Ser Ala Asp Gln Thr Thr Gly Tyr Arg Ser Ala Ala Leu
 125 130 135 140
 gga gtt gat tct ctc att gat gca gta ccc caa ttg tgc aat gta gcc 544
 Gly Val Asp Ser Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ala
 145 150 155
 aat gtg aga ggt gtc cag ttt gcc aac acg gac agc ata gac atg agc 592

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Asn	Val	Arg	Gly 160	Val	Gln	Phe	Ala	Asn 165	Thr	Asp	Ser	Ile	Asp 170	Met	Ser
tcg	gcc	atg	ttg	agg	act	ttg	gcg	aag	cag	atc	cag	aat	gat	ctg	gac
Ser	Ala	Met 175	Leu	Arg	Thr	Leu	Ala 180	Lys	Gln	Ile	Gln	Asn 185	Asp	Leu	Asp
640															
agt	ccg	ttt	act	caa	ggc	gca	ggt	gtg	acg	cac	gga	act	gat	act	ctg
Ser	Pro 190	Phe	Thr	Gln	Gly	Ala 195	Val	Val	Thr	His	Gly 200	Thr	Asp	Thr	Leu
688															
gat	gaa	tct	gcc	ttc	ttt	ctg	gat	ctt	act	atc	cag	agc	gac	aag	ccc
Asp 205	Glu	Ser	Ala	Phe	Phe 210	Leu	Asp	Leu	Thr	Ile 215	Gln	Ser	Asp	Lys	Pro 220
736															
gtg	gtc	gtg	aca	ggc	tca	atg	cgc	ccg	gca	act	gct	atc	agc	gca	gat
Val	Val	Val	Thr	Gly 225	Ser	Met	Arg	Pro	Ala 230	Thr	Ala	Ile	Ser	Ala 235	Asp
784															
gga	cca	atg	aat	ctt	ttg	tca	tcg	gtg	aca	ttg	gca	gca	gca	gcg	agt
Gly	Pro	Met	Asn 240	Leu	Leu	Ser	Ser	Val 245	Thr	Leu	Ala	Ala	Ala 250	Ala	Ser
832															
gct	cga	ggc	aga	gga	gtg	atg	att	gcc	atg	aat	gat	cgc	att	gga	tct
Ala	Arg	Gly 255	Arg	Gly	Val	Met	Ile 260	Ala	Met	Asn	Asp	Arg 265	Ile	Gly	Ser
880															
gct	cgt	ttt	acg	acc	aaa	gtc	aac	gcc	aac	cat	ttg	gac	gcc	ttc	caa
Ala	Arg 270	Phe	Thr	Thr	Lys	Val 275	Asn	Ala	Asn	His	Leu 280	Asp	Ala	Phe	Gln
928															
gcc	cct	gac	agt	ggc	atg	ctg	gga	aca	ttc	gtc	aac	gtt	cag	cca	gtg
Ala 285	Pro	Asp	Ser	Gly	Met 290	Leu	Gly	Thr	Phe	Val 295	Asn	Val	Gln	Pro	Val 300
976															
ttt	ttc	tat	ccg	cca	tca	cga	cct	ctt	ggc	cac	cgt	cat	ttt	gat	ctg
Phe	Phe	Tyr	Pro	Pro 305	Ser	Arg	Pro	Leu	Gly 310	His	Arg	His	Phe	Asp 315	Leu
1024															
cgg	ccc	atc	acc	aac	aac	ggc	cgc	cgg	ttc	gga	cgc	tct	aca	gcc	ccc
Arg	Pro	Ile	Thr 320	Asn	Asn	Gly	Arg	Arg 325	Phe	Gly	Arg	Ser	Thr 330	Ala	Pro
1072															
gga	gca	gga	tca	tca	gca	cta	ccc	cag	gtg	gac	gtg	ctc	tac	gct	tac
Gly	Ala	Gly 335	Ser	Ser	Ala	Leu	Pro 340	Gln	Val	Asp	Val	Leu 345	Tyr	Ala	Tyr
1120															
cag	gag	ctc	agc	gtg	ggc	atg	ttc	cag	gcg	gcc	atc	gac	ctt	gga	gcg
Gln	Glu 350	Leu	Ser	Val	Gly	Met 355	Phe	Gln	Ala	Ala	Ile 360	Asp	Leu	Gly	Ala
1168															
cag	ggc	atc	gtt	cta	gcg	gga	atg	ggc	gct	gga	ttc	tgg	acg	tcc	aaa
Gln 365	Gly	Ile	Val	Leu	Ala 370	Gly	Met	Gly	Ala	Gly 375	Phe	Trp	Thr	Ser	Lys 380
1216															
ggt	acc	gag	gag	att	cgg	cgt	atc	gtc	cac	gag	acc	gat	att	ccc	gtg
Gly	Thr	Glu	Glu	Ile 385	Arg	Arg	Ile	Val	His 390	Glu	Thr	Asp	Ile	Pro 395	Val
1264															
ata	gtg	agc	cga	aga	ccg	gaa	ggc	ggc	ttc	gtc	gga	cca	tgt	gag	gca
Ile	Val	Ser	Arg 400	Arg	Pro	Glu	Gly	Gly 405	Phe	Val	Gly	Pro	Cys 410	Glu	Ala
1312															
gga	atc	ggc	gcg	ggc	ttt	ttg	aat	ccg	caa	aag	gcg	agg	atc	cag	ctc
Gly	Ile	Gly 415	Ala	Gly	Phe	Leu	Asn 420	Pro	Gln	Lys	Ala	Arg 425	Ile	Gln	Leu
1360															
caa	ctg	gcc	ctg	gag	acc	aag	atg	gac	aat	gat	gcc	atc	aaa	gcc	ctg
1408															

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Gln Leu Ala Leu Glu Thr Lys Met Asp Asn Asp Ala Ile Lys Ala Leu
 430 435 440

ttt gag cat tcg gga gtg cac taaagggaca aaaaagatcg aggttacagc 1459
 Phe Glu His Ser Gly Val His
 445 450

agcaacacca c 1470

<210> 10
 <211> 451
 <212> PRT
 <213> Fusarium graminearum

<400> 10

Met Met Pro Ser Val Arg Arg Phe His Gly Gln Thr Met Val Ala Ala
 1 5 10 15

Ala Pro Ser Ile Cys Ser Gly Pro Ala Ala Ser Ser Thr Ile Lys Met
 20 25 30

Ala Ser Ser Ser Ala Ser Trp Thr Thr Tyr Leu Trp Arg Leu Ile Leu
 35 40 45

Ala Val Leu Ala Pro Ser Thr Ala Leu Leu Pro Phe Gly Ala Trp Val
 50 55 60

Val Ser Val Trp Gly Ser Pro Val Leu Asp Leu His Val Gln Pro His
 65 70 75 80

Phe Ser Val Gln Gln Lys Ala Pro Ile Gln Thr Gly Ile Pro Phe Glu
 85 90 95

Ile Ser Thr Thr Ser Gly Phe Asn Cys Phe Asn Pro Asn Leu Pro Asn
 100 105 110

Val Thr Ile Tyr Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Ser Ser
 115 120 125

Ala Asp Gln Thr Thr Gly Tyr Arg Ser Ala Ala Leu Gly Val Asp Ser
 130 135 140

Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ala Asn Val Arg Gly
 145 150 155 160

Val Gln Phe Ala Asn Thr Asp Ser Ile Asp Met Ser Ser Ala Met Leu
 165 170 175

Arg Thr Leu Ala Lys Gln Ile Gln Asn Asp Leu Asp Ser Pro Phe Thr
 180 185 190

Gln Gly Ala Val Val Thr His Gly Thr Asp Thr Leu Asp Glu Ser Ala
 195 200 205

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Phe Phe Leu Asp Leu Thr Ile Gln Ser Asp Lys Pro Val Val Val Thr
 210 215 220
 Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Met Asn
 225 230 235 240
 Leu Leu Ser Ser Val Thr Leu Ala Ala Ala Ala Ser Ala Arg Gly Arg
 245 250 255
 Gly Val Met Ile Ala Met Asn Asp Arg Ile Gly Ser Ala Arg Phe Thr
 260 265 270
 Thr Lys Val Asn Ala Asn His Leu Asp Ala Phe Gln Ala Pro Asp Ser
 275 280 285
 Gly Met Leu Gly Thr Phe Val Asn Val Gln Pro Val Phe Phe Tyr Pro
 290 295 300
 Pro Ser Arg Pro Leu Gly His Arg His Phe Asp Leu Arg Pro Ile Thr
 305 310 315 320
 Asn Asn Gly Arg Arg Phe Gly Arg Ser Thr Ala Pro Gly Ala Gly Ser
 325 330 335
 Ser Ala Leu Pro Gln Val Asp Val Leu Tyr Ala Tyr Gln Glu Leu Ser
 340 345 350
 Val Gly Met Phe Gln Ala Ala Ile Asp Leu Gly Ala Gln Gly Ile Val
 355 360 365
 Leu Ala Gly Met Gly Ala Gly Phe Trp Thr Ser Lys Gly Thr Glu Glu
 370 375 380
 Ile Arg Arg Ile Val His Glu Thr Asp Ile Pro Val Ile Val Ser Arg
 385 390 395 400
 Arg Pro Glu Gly Gly Phe Val Gly Pro Cys Glu Ala Gly Ile Gly Ala
 405 410 415
 Gly Phe Leu Asn Pro Gln Lys Ala Arg Ile Gln Leu Gln Leu Ala Leu
 420 425 430
 Glu Thr Lys Met Asp Asn Asp Ala Ile Lys Ala Leu Phe Glu His Ser
 435 440 445
 Gly Val His
 450

<210> 11
 <211> 1236
 <212> DNA

10347-WO-ST25

<213> Penicillium citrinum

<220>

<221> CDS

<222> (16)..(1152)

<400> 11

acatattgaa acaat	atg aga ctt cta ttt aat act ctg gct gtc tca gca	51
	Met Arg Leu Leu Phe Asn Thr Leu Ala Val Ser Ala	
	1 5 10	
cta gct gct acg agt tat gcc tct ccc atc att cat tcc cgg gcc tcc	99	
Leu Ala Ala Thr Ser Tyr Ala Ser Pro Ile Ile His Ser Arg Ala Ser		
	15 20 25	
aac acg tcc tat acc aac tct aat ggg ctg aaa ttt aac cat ttc gac	147	
Asn Thr Ser Tyr Thr Asn Ser Asn Gly Leu Lys Phe Asn His Phe Asp		
	30 35 40	
gct tct ctt cca aat gtg act ttg ctg gca act ggt gga act att gcc	195	
Ala Ser Leu Pro Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala		
	45 50 55 60	
ggt aca agc gat gac aag act gct acg gca gga tat gaa tcc ggg gct	243	
Gly Thr Ser Asp Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala		
	65 70 75	
tta ggg ata aat aag att ctt tcc ggc atc cca gaa gtt tat gac att	291	
Leu Gly Ile Asn Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile		
	80 85 90	
gcc aac gtc aat gcg gta cag ttt gac aat gtc aac agc ggc gat gtc	339	
Ala Asn Val Asn Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val		
	95 100 105	
tct yca tct ctc tta ctg aac atg aca cat acc ctt caa aag acc gtt	387	
Ser Xaa Ser Leu Leu Leu Asn Met Thr His Thr Leu Gln Lys Thr Val		
	110 115 120	
tgt gat gac cct acg ata tct ggc gcc gtc atc acc cat ggc acc gat	435	
Cys Asp Asp Pro Thr Ile Ser Gly Ala Val Ile Thr His Gly Thr Asp		
	125 130 135 140	
acc ctg gaa gaa tct gcc ttc ttc atc gat gca aca gtc aac tgc ggc	483	
Thr Leu Glu Glu Ser Ala Phe Phe Ile Asp Ala Thr Val Asn Cys Gly		
	145 150 155	
aag ccg att gtg ttc gtt ggc tca atg cga cct tcc acc gca atc tct	531	
Lys Pro Ile Val Phe Val Gly Ser Met Arg Pro Ser Thr Ala Ile Ser		
	160 165 170	
gcc gat ggc cct atg aat ttg ctc cag gga gtg act gtg gcc gct gac	579	
Ala Asp Gly Pro Met Asn Leu Leu Gln Gly Val Thr Val Ala Ala Asp		
	175 180 185	
aaa cag gct aag aac cgc gga gca cta gtc gtg ctg aat gac cgc att	627	
Lys Gln Ala Lys Asn Arg Gly Ala Leu Val Val Leu Asn Asp Arg Ile		
	190 195 200	
gtc tct gct ttc ttc gct aca aag aca aat gcg aat aca atg gac act	675	
Val Ser Ala Phe Phe Ala Thr Lys Thr Asn Ala Asn Thr Met Asp Thr		
	205 210 215 220	
ttc aag gct tat gaa caa ggc agt ctt ggc atg att gtt tca aac aag	723	
Phe Lys Ala Tyr Glu Gln Gly Ser Leu Gly Met Ile Val Ser Asn Lys		
	225 230 235	

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ccc tac ttc tat tat ccg gca gtc gag cca aac gcg aag cac gtt gtt      771
Pro Tyr Phe Tyr Tyr Pro Ala Val Glu Pro Asn Ala Lys His Val Val
                240                245                250

cat ctt gac gac gtg gat gcg atc ccc cgt gtg gat att ctc tac gct      819
His Leu Asp Asp Val Asp Ala Ile Pro Arg Val Asp Ile Leu Tyr Ala
                255                260                265

tac gag gac atg cat agc gac tcc ctt cac agt gct atc aaa aat gga      867
Tyr Glu Asp Met His Ser Asp Ser Leu His Ser Ala Ile Lys Asn Gly
                270                275                280

gcc aag ggc atc gtg gtc gcc ggc gag ggc gca ggt ggt atc tcc acg      915
Ala Lys Gly Ile Val Val Ala Gly Glu Gly Ala Gly Gly Ile Ser Thr
285                290                295                300

gac ttt agt gat acc atc gat gag att gca tcg aag cat cag att ccc      963
Asp Phe Ser Asp Thr Ile Asp Glu Ile Ala Ser Lys His Gln Ile Pro
                305                310                315

att atc ctg agc cac aga acc gtg aac gga gaa gtt cct act gct gat     1011
Ile Ile Leu Ser His Arg Thr Val Asn Gly Glu Val Pro Thr Ala Asp
                320                325                330

att acg ggt gat agc gcg aag act cgc att gca agt ggc atg tat aac     1059
Ile Thr Gly Asp Ser Ala Lys Thr Arg Ile Ala Ser Gly Met Tyr Asn
                335                340                345

ccc cag cag gcg cgc gtc ttg ctt gga cta ttg ctc gca gaa ggc aag     1107
Pro Gln Gln Ala Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys
                350                355                360

aag ttt gag gat att cga act atc ttc gga aaa gct act gtt gcc      1152
Lys Phe Glu Asp Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala
365                370                375

tagaccacg tcatatatta tgccatact tgggaaact tgaaactgat agactaaatt     1212
aattatattg tcgtttgttg ccgg                                           1236

```

<210> 12
 <211> 379
 <212> PRT
 <213> Penicillium citrinum

<220>
 <221> misc_feature
 <222> (110)..(110)
 <223> The 'xaa' at location 110 stands for Pro, or Ser.

<400> 12

Met Arg Leu Leu Phe Asn Thr Leu Ala Val Ser Ala Leu Ala Ala Thr
1 5 10 15

Ser Tyr Ala Ser Pro Ile Ile His Ser Arg Ala Ser Asn Thr Ser Tyr
20 25 30

Thr Asn Ser Asn Gly Leu Lys Phe Asn His Phe Asp Ala Ser Leu Pro
35 40 45

Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala Gly Thr Ser Asp
50 55 60

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Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala Leu Gly Ile Asn
 65 70 75 80
 Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile Ala Asn Val Asn
 85 90 95
 Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val Ser Xaa Ser Leu
 100 105 110
 Leu Leu Asn Met Thr His Thr Leu Gln Lys Thr Val Cys Asp Asp Pro
 115 120 125
 Thr Ile Ser Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
 130 135 140
 Ser Ala Phe Phe Ile Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
 145 150 155 160
 Phe Val Gly Ser Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
 165 170 175
 Met Asn Leu Leu Gln Gly Val Thr Val Ala Ala Asp Lys Gln Ala Lys
 180 185 190
 Asn Arg Gly Ala Leu Val Val Leu Asn Asp Arg Ile Val Ser Ala Phe
 195 200 205
 Phe Ala Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Tyr
 210 215 220
 Glu Gln Gly Ser Leu Gly Met Ile Val Ser Asn Lys Pro Tyr Phe Tyr
 225 230 235 240
 Tyr Pro Ala Val Glu Pro Asn Ala Lys His Val Val His Leu Asp Asp
 245 250 255
 Val Asp Ala Ile Pro Arg Val Asp Ile Leu Tyr Ala Tyr Glu Asp Met
 260 265 270
 His Ser Asp Ser Leu His Ser Ala Ile Lys Asn Gly Ala Lys Gly Ile
 275 280 285
 Val Val Ala Gly Glu Gly Ala Gly Gly Ile Ser Thr Asp Phe Ser Asp
 290 295 300
 Thr Ile Asp Glu Ile Ala Ser Lys His Gln Ile Pro Ile Ile Leu Ser
 305 310 315 320
 His Arg Thr Val Asn Gly Glu Val Pro Thr Ala Asp Ile Thr Gly Asp
 325 330 335

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Ser Ala Lys Thr Arg Ile Ala Ser Gly Met Tyr Asn Pro Gln Gln Ala
 340 345 350

Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys Lys Phe Glu Asp
 355 360 365

Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala
 370 375

<210> 13

<211> 362

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 13

Met Arg Ser Leu Asn Thr Leu Leu Leu Ser Leu Phe Val Ala Met Ser
 1 5 10 15

Ser Gly Ala Pro Leu Leu Lys Ile Arg Glu Glu Lys Asn Ser Ser Leu
 20 25 30

Pro Ser Ile Lys Ile Phe Gly Thr Gly Gly Thr Ile Ala Ser Lys Gly
 35 40 45

Ser Thr Ser Ala Thr Thr Ala Gly Tyr Ser Val Gly Leu Thr Val Asn
 50 55 60

Asp Leu Ile Glu Ala Val Pro Ser Leu Ala Glu Lys Ala Asn Leu Asp
 65 70 75 80

Tyr Leu Gln Val Ser Asn Val Gly Ser Asn Ser Leu Asn Tyr Thr His
 85 90 95

Leu Ile Pro Leu Tyr His Gly Ile Ser Glu Ala Leu Ala Ser Asp Asp
 100 105 110

Tyr Ala Gly Ala Val Val Thr His Gly Thr Asp Thr Met Glu Glu Thr
 115 120 125

Ala Phe Phe Leu Asp Leu Thr Ile Asn Ser Glu Lys Pro Val Cys Ile
 130 135 140

Ala Gly Ala Met Arg Pro Ala Thr Ala Thr Ser Ala Asp Gly Pro Met
 145 150 155 160

Asn Leu Tyr Gln Ala Val Ser Ile Ala Ala Ser Glu Lys Ser Leu Gly
 165 170 175

Arg Gly Thr Met Ile Thr Leu Asn Asp Arg Ile Ala Ser Gly Phe Trp
 180 185 190

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Thr Thr Lys Met Asn Ala Asn Ser Leu Asp Thr Phe Arg Ala Asp Glu
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Gln Gly Tyr Leu Gly Tyr Phe Ser Asn Asp Asp Val Glu Phe Tyr Tyr
 210 215 220

Pro Pro Val Lys Pro Asn Gly Trp Gln Phe Phe Asp Ile Ser Asn Leu
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Thr Asp Pro Ser Glu Ile Pro Glu Val Ile Ile Leu Tyr Ser Tyr Gln
 245 250 255

Gly Leu Asn Pro Glu Leu Ile Val Lys Ala Val Lys Asp Leu Gly Ala
 260 265 270

Lys Gly Ile Val Leu Ala Gly Ser Gly Ala Gly Ser Trp Thr Ala Thr
 275 280 285

Gly Ser Ile Val Asn Glu Gln Leu Tyr Glu Glu Tyr Gly Ile Pro Ile
 290 295 300

Val His Ser Arg Arg Thr Ala Asp Gly Thr Val Pro Pro Asp Asp Ala
 305 310 315 320

Pro Glu Tyr Ala Ile Gly Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
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Arg Ser Val Phe Ser Gly Val Tyr Gly Gly
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28